36

SEQUENCE LISTING

(1) GENERAL INFORMATION:
   (i) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO. 1:
   (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 3884 base pairs
      (B)   TYPE: nucleic acid and amino acid
      (C)   STRANDEDNESS: double
      (D)   TOPOLOGY: linear

   (ii) MOLECULAR TYPE: cDNA
   (vi) ORIGINAL SOURCE:
      (E)   ORGANISM: human
      (F)   CELLTYPE: chondrocyte
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

```
        CAGGTCAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTG
    1   ---------+---------+---------+---------+---------+---------+  60
        GTCCAGTCTTTGGCTAGTCCGTACCTTGAGGGGAAGCAGTGAGTGGACAAGAACGGGGAC

a                        M  E  L  P  F  V  T  H  L  F  L  P  L   -

        GTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTC
   61   ---------+---------+---------+---------+---------+---------+  120
        CACAAGGACTGTCCAGAGACGAGGGGGAAATTGGACCTACTTGTAGTGGGTGCGGATAAG

a        V  F  L  T  G  L  C  S  P  F  N  L  D  E  H  H  P  R  L  F   -

        CCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAG
  121   ---------+---------+---------+---------+---------+---------+  180
        GGTCCCGGTGGTCTTCGACTTAAACCTATGTCACAGAATGTTGTACAACCCCCACCTGTC

a        P  G  P  P  E  A  E  F  G  Y  S  V  L  Q  H  V  G  G  G  Q   -

        CGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
  181   ---------+---------+---------+---------+---------+---------+  240
        GCTACCTACGACCACCCGCGGGGGACCCTACCCGGAAGTCCGCTGGCCTCCCCCCTGCAA

a        R  W  M  L  V  G  A  P  W  D  G  P  S  G  D  R  R  G  D  V   -

        TATCGCTGCCCTGTAGGGGGGGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGAC
  241   ---------+---------+---------+---------+---------+---------+  300
        ATAGCGACGGGACATCCCCCCCGGGTGTTACGGGGTACACGGTTCCCGGTGAATCCACTG

a        Y  R  C  P  V  G  G  A  H  N  A  P  C  A  K  G  H  L  G  D   -

        TACCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTA
  301   ---------+---------+---------+---------+---------+---------+  360
        ATGGTTGACCCTTTAAGTAGAGTAGGACGACACTTATACGTGGACCCCTACAGAGACAAT

a        Y  Q  L  G  N  S  S  H  P  A  V  N  M  H  L  G  M  S  L  L   -

        GAGACAGATGGTGATGGGGGATTCATGGCCTGTGCCCCTCTCTGGTCTCGTGCTTGTGGC
  361   ---------+---------+---------+---------+---------+---------+  420
        CTCTGTCTACCACTACCCCCTAAGTACCGGACACGGGGAGAGACCAGAGCACGAACACCG

a        E  T  D  G  D  G  G  F  M  A  C  A  P  L  W  S  R  A  C  G   -
```

37

```
        AGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGA
    421 ---------+---------+---------+---------+---------+---------+ 480
        TCGAGACAGAAGTCAAGACCCTATACACGGGCACACCTACGAAGTAAGGTCGGAGTCCCT

    a    S  S  V  F  S  S  G  I  C  A  R  V  D  A  S  F  Q  P  Q  G  -

        AGCCTGGCACCCACTGCCCAACGCTGCCCAACATACATGGATGTTGTCATTGTCTTGGAT
    481 ---------+---------+---------+---------+---------+---------+ 540
        TCGGACCGTGGGTGACGGGTTGCGACGGGTTGTATGTACCTACAACAGTAACAGAACCTA

    a    S  L  A  P  T  A  Q  R  C  P  T  Y  M  D  V  V  I  V  L  D  -

        GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGACCTTCCTACGAAGACTGGTAGGG
    541 ---------+---------+---------+---------+---------+---------+ 600
        CCGAGGTTGTCGTAGATGGGGACCAGACTTCAAGTCTGGAAGGATGCTTCTGACCATCCC

    a    G  S  N  S  I  Y  P  W  S  E  V  Q  T  F  L  R  R  L  V  G  -

        AAACTGTTTATTGACCCAGAACAGATACAGGTGGGACTGGTACAGTATGGGGAGAGCCCT
    601 ---------+---------+---------+---------+---------+---------+ 660
        TTTGACAAATAACTGGGTCTTGTCTATGTCCACCCTGACCATGTCATACCCCTCTCGGGA

    a    K  L  F  I  D  P  E  Q  I  Q  V  G  L  V  Q  Y  G  E  S  P  -

        GTACATGAGTGGTCCCTGGGAGATTTCCGAACGAAGGAAGAAGTGGTGAGAGCAGCAAAG
    661 ---------+---------+---------+---------+---------+---------+ 720
        CATGTACTCACCAGGGACCCTCTAAAGGCTTGCTTCCTTCTTCACCACTCTCGTCGTTTC

    a    V  H  E  W  S  L  G  D  F  R  T  K  E  E  V  V  R  A  A  K  -

        AACCTCAGTCGGCGGGAGGGACGAGAAACAAAGACTGCCCAAGCAATAATGGTGGCCTGC
    721 ---------+---------+---------+---------+---------+---------+ 780
        TTGGAGTCAGCCGCCCTCCCTGCTCTTTGTTTCTGACGGGTTCGTTATTACCACCGGACG

    a    N  L  S  R  R  E  G  R  E  T  K  T  A  Q  A  I  M  V  A  C  -

        ACAGAAGGGTTCAGTCAGTCCCATGGGGGCCGACCCGAGGCTGCCAGGCTACTGGTGGTT
    781 ---------+---------+---------+---------+---------+---------+ 840
        TGTCTTCCCAAGTCAGTCAGGGTACCCCCGGCTGGGCTCCGACGGTCCGATGACCACCAA

    a    T  E  G  F  S  Q  S  H  G  G  R  P  E  A  A  R  L  L  V  V  -

        GTCACTGATGGAGAGTCCCATGATGGAGAGGAGCTTCCTGCAGCACTAAAGGCCTGTGAG
    841 ---------+---------+---------+---------+---------+---------+ 900
        CAGTGACTACCTCTCAGGGTACTACCTCTCCTCGAAGGACGTCGTGATTTCCGGACACTC

    a    V  T  D  G  E  S  H  D  G  E  E  L  P  A  A  L  K  A  C  E  -

        GCTGGAAGAGTGACACGCTATGGGATTGCAGTCCTTGGTCACTACCTCCGGCGGCAGCGA
    901 ---------+---------+---------+---------+---------+---------+ 960
        CGACCTTCTCACTGTGCGATACCCTAACGTCAGGAACCAGTGATGGAGGCCGCCGTCGCT

    a    A  G  R  V  T  R  Y  G  I  A  V  L  G  H  Y  L  R  R  Q  R  -

        GATCCCAGCTCTTTCCTGAGAGAAATTAGAACTATTGCCAGTGATCCAGATGAGCGATTC
    961 ---------+---------+---------+---------+---------+---------+ 1020
        CTAGGGTCGAGAAAGGACTCTCTTTAATCTTGATAACGGTCACTAGGTCTACTCGCTAAG

    a    D  P  S  S  F  L  R  E  I  R  T  I  A  S  D  P  D  E  R  F  -

        TTCTTCAATGTCACAGATGAGGCTGCTCTGACTGACATTGTGGATGCACTAGGAGATCGG
   1021 ---------+---------+---------+---------+---------+---------+ 1080
        AAGAAGTTACAGTGTCTACTCCGACGAGACTGACTGTAACACCTACGTGATCCTCTAGCC

    a    F  F  N  V  T  D  E  A  A  L  T  D  I  V  D  A  L  G  D  R  -
```

```
        ATTTTTGGCCTTGAAGGGTCCCATGCAGAAAACGAAAGCTCCTTTGGGCTGGAAATGTCT
   1081 ---------+---------+---------+---------+---------+---------+ 1140
        TAAAAACCGGAACTTCCCAGGGTACGTCTTTTGCTTTCGAGGAAACCCGACCTTTACAGA

      a    I  F  G  L  E  G  S  H  A  E  N  E  S  S  F  G  L  E  M  S  -

        CAGATTGGTTTCTCCACTCATCGGCTAAAGGATGGGATTCTTTTTGGGATGGTGGGGGCC
   1141 ---------+---------+---------+---------+---------+---------+ 1200
        GTCTAACCAAAGAGGTGAGTAGCCGATTTCCTACCCTAAGAAAAACCCTACCACCCCCGG

      a    Q  I  G  F  S  T  H  R  L  K  D  G  I  L  F  G  M  V  G  A  -

        TATGACTGGGGAGGCTCTGTGCTATGGCTTGAAGGAGGCCACCGCCTTTTCCCCCCACGA
   1201 ---------+---------+---------+---------+---------+---------+ 1260
        ATACTGACCCCTCCGAGACACGATACCGAACTTCCTCCGGTGGCGGAAAAGGGGGGTGCT

      a    Y  D  W  G  G  S  V  L  W  L  E  G  G  H  R  L  F  P  P  R  -

        ATGGCACTGGAAGACGAGTTCCCCCCTGCACTGCAGAACCATGCAGCCTACCTGGGTTAC
   1261 ---------+---------+---------+---------+---------+---------+ 1320
        TACCGTGACCTTCTGCTCAAGGGGGGACGTGACGTCTTGGTACGTCGGATGGACCCAATG

      a    M  A  L  E  D  E  F  P  P  A  L  Q  N  H  A  A  Y  L  G  Y  -

        TCTGTTTCTTCCATGCTTTTGCGGGGTGGACGCCGCCTGTTTCTCTCTGGGGCTCCTCGA
   1321 ---------+---------+---------+---------+---------+---------+ 1380
        AGACAAAGAAGGTACGAAAACGCCCCACCTGCGGCGGACAAAGAGAGACCCCGAGGAGCT

      a    S  V  S  S  M  L  L  R  G  G  R  R  L  F  L  S  G  A  P  R  -

        TTTAGACATCGAGGAAAAGTCATCGCCTTCCAGCTTAAGAAAGATGGGGCTGTGAGGGTT
   1381 ---------+---------+---------+---------+---------+---------+ 1440
        AAATCTGTAGCTCCTTTTCAGTAGCGGAAGGTCGAATTCTTTCTACCCCGACACTCCCAA

      a    F  R  H  R  G  K  V  I  A  F  Q  L  K  K  D  G  A  V  R  V  -

        GCCCAGAGCCTCCAGGGGGAGCAGATTGGTTCATACTTTGGCAGTGAGCTCTGCCCATTG
   1441 ---------+---------+---------+---------+---------+---------+ 1500
        CGGGTCTCGGAGGTCCCCCTCGTCTAACCAAGTATGAAACCGTCACTCGAGACGGGTAAC

      a    A  Q  S  L  Q  G  E  Q  I  G  S  Y  F  G  S  E  L  C  P  L  -

        GATACAGATAGGGATGGAACAACTGATGTCTTACTTGTGGCTGCCCCCATGTTCCTGGGA
   1501 ---------+---------+---------+---------+---------+---------+ 1560
        CTATGTCTATCCCTACCTTGTTGACTACAGAATGAACACCGACGGGGGTACAAGGACCCT

      a    D  T  D  R  D  G  T  T  D  V  L  L  V  A  A  P  M  F  L  G  -

        CCCCAGAACAAGGAAACAGGACGTGTTTATGTGTATCTGGTAGGCCAGCAGTCCTTGCTG
   1561 ---------+---------+---------+---------+---------+---------+ 1620
        GGGGTCTTGTTCCTTTGTCCTGCACAAATACACATAGACCATCCGGTCGTCAGGAACGAC

      a    P  Q  N  K  E  T  G  R  V  Y  V  Y  L  V  G  Q  Q  S  L  L  -

        ACCCTCCAAGGAACACTTCAGCCAGAACCCCCCCAGGATGCTCGGTTTGGCTTTGCCATG
   1621 ---------+---------+---------+---------+---------+---------+ 1680
        TGGGAGGTTCCTTGTGAAGTCGGTCTTGGGGGGGTCCTACGAGCCAAACCGAAACGGTAC

      a    T  L  Q  G  T  L  Q  P  E  P  P  Q  D  A  R  F  G  F  A  M  -

        GGAGCTCTTCCTGATCTGAACCAAGATGGTTTTGCTGATGTGGCTGTGGGGGCGCCTCTG
   1681 ---------+---------+---------+---------+---------+---------+ 1740
        CCTCGAGAAGGACTAGACTTGGTTCTACCAAAACGACTACACCGACACCCCGCGGAGAC

      a    G  A  L  P  D  L  N  Q  D  G  F  A  D  V  A  V  G  A  P  L  -
```

```
      GAAGATGGGCACCAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCCC
1741  ---------+---------+---------+---------+---------+---------+ 1800
      CTTCTACCCGTGGTCCCTCGTGACATGGACATGGTACCTTGGGTCTCACCTCAGTCCGGG

a       E   D   G   H   Q   G   A   L   Y   L   Y   H   G   T   Q   S   G   V   R   P   -

      CATCCTGCCCAGAGGATTGCTGCTGCCTCCATGCCACATGCCCTCAGCTACTTTGGCCGA
1801  ---------+---------+---------+---------+---------+---------+ 1860
      GTAGGACGGGTCTCCTAACGACGACGGAGGTACGGTGTACGGGAGTCGATGAAACCGGCT

a       H   P   A   Q   R   I   A   A   A   S   M   P   H   A   L   S   Y   F   G   R   -

      AGTGTGGATGGTCGGCTAGATCTGGATGGAGATGATCTGGTCGATGTGGCTGTGGGTGCC
1861  ---------+---------+---------+---------+---------+---------+ 1920
      TCACACCTACCAGCCGATCTAGACCTACCTCTACTAGACCAGCTACACCGACACCCACGG

a       S   V   D   G   R   L   D   L   D   G   D   D   L   V   D   V   A   V   G   A   -

      CAGGGGGCAGCCATCCTGCTCAGCTCCCGGCCCATTGTCCATCTGACCCCATCACTGGAG
1921  ---------+---------+---------+---------+---------+---------+ 1980
      GTCCCCCGTCGGTAGGACGAGTCGAGGGCCGGGTAACAGGTAGACTGGGGTAGTGACCTC

a       Q   G   A   A   I   L   S   S   R   P   I   V   H   L   T   P   S   L   E   -

      GTGACCCCACAGGCCATCAGTGTGGTTCAGAGGGACTGTAGGCGGCGAGGCCAAGAAGCA
1981  ---------+---------+---------+---------+---------+---------+ 2040
      CACTGGGGTGTCCGGTAGTCACACCAAGTCTCCCTGACATCCGCCGCTCCGGTTCTTCGT

a       V   T   P   Q   A   I   S   V   V   Q   R   D   C   R   R   R   G   Q   E   A   -

      GTCTGTCTGACTGCAGCCCTTTGCTTCCAAGTGACCTCCCGTACTCCTGGTCGCTGGGAT
2041  ---------+---------+---------+---------+---------+---------+ 2100
      CAGACAGACTGACGTCGGGAAACGAAGGTTCACTGGAGGGCATGAGGACCAGCGACCCTA

a       V   C   L   T   A   A   L   C   F   Q   V   T   S   R   T   P   G   R   W   D   -

      CACCAATTCTACATGAGGTTCACCGCATCACTGGATGAATGGACTGCTGGGGCACGTGCA
2101  ---------+---------+---------+---------+---------+---------+ 2160
      GTGGTTAAGATGTACTCCAAGTGGCGTAGTGACCTACTTACCTGACGACCCCGTGCACGT

a       H   Q   F   Y   M   R   F   T   A   S   L   D   E   W   T   A   G   A   R   A   -

      GCATTTGATGGCTCTGGCCAGAGGTTGTCCCCTCGGAGGCTCCGGCTCAGTGTGGGGAAT
2161  ---------+---------+---------+---------+---------+---------+ 2220
      CGTAAACTACCGAGACCGGTCTCCAACAGGGGAGCCTCCGAGGCCGAGTCACACCCCTTA

a       A   F   D   G   S   G   Q   R   L   S   R   R   R   L   R   L   S   V   G   N   -

      GTCACTTGTGAGCAGCTACACTTCCATGTGCTGGATACATCAGATTACCTCCGGCCAGTG
2221  ---------+---------+---------+---------+---------+---------+ 2280
      CAGTGAACACTCGTCGATGTGAAGGTACACGACCTATGTAGTCTAATGGAGGCCGGTCAC

a       V   T   C   E   Q   L   H   F   H   V   L   D   T   S   D   Y   L   R   P   V   -

      GCCTTGACTGTGACCTTTGCCTTGGACAATACTACAAAGCCAGGGCCTGTGCTGAATGAG
2281  ---------+---------+---------+---------+---------+---------+ 2340
      CGGAACTGACACTGGAAACGGAACCTGTTATGATGTTTCGGTCCCGGACACGACTTACTC

a       A   L   T   V   T   F   A   L   D   N   T   T   K   P   G   P   V   L   N   E   -

      GGCTCACCCACCTCTATACAAAAGCTGGTCCCCTTCTCAAAGGATTGTGGCCCTGACAAT
2341  ---------+---------+---------+---------+---------+---------+ 2400
      CCGAGTGGGTGGAGATATGTTTTCGACCAGGGGAAGAGTTTCCTAACACCGGGACTGTTA

a       G   S   P   T   S   I   Q   K   L   V   P   F   S   K   D   C   G   P   D   N   -
```

```
      GAATGTGTCACAGACCTGGTGCTTCAAGTGAATATGGACATCAGAGGCTCCAGGAAGGCC
2401  ----------+---------+---------+---------+---------+---------+  2460
      CTTACACAGTGTCTGGACCACGAAGTTCACTTATACCTGTAGTCTCCGAGGTCCTTCCGG

   a     E  C  V  T  D  L  V  L  Q  V  N  M  D  I  R  G  S  R  K  A  -

      CCATTTGTGGTTCGAGGTGGCCGGCGGAAAGTGCTGGTATCTACAACTCTGGAGAACAGA
2461  ----------+---------+---------+---------+---------+---------+  2520
      GGTAAACACCAAGCTCCACCGGCCGCCTTTCACGACCATAGATGTTGAGACCTCTTGTCT

   a     P  F  V  V  R  G  G  R  R  K  V  L  V  S  T  T  L  E  N  R  -

      AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTTCTCTAGAAACCTCCACCTGGCC
2521  ----------+---------+---------+---------+---------+---------+  2580
      TTCCTTTTACGAATGTTATGCTCGGACTCATAGTAGAAGAGATCTTTGGAGGTGGACCGG

   a     K  E  N  A  Y  N  T  S  L  S  I  I  F  S  R  N  L  H  L  A  -

      AGTCTCACTCCTCAGAGAGAGAGCCCAATAAAGGTGGAATGTGCCGCCCCTTCTGCTCAT
2581  ----------+---------+---------+---------+---------+---------+  2640
      TCAGAGTGAGGAGTCTCTCTCTCGGGTTATTTCCACCTTACACGGCGGGGAAGACGAGTA

   a     S  L  T  P  Q  R  E  S  P  I  K  V  E  C  A  A  P  S  A  H  -

      GCCCGGCTCTGCAGTGTGGGGCATCCTGTCTTCCAGACTGGAGCCAAGGTGACCTTTCTG
2641  ----------+---------+---------+---------+---------+---------+  2700
      CGGGCCGAGACGTCACACCCCGTAGGACAGAAGGTCTGACCTCGGTTCCACTGGAAAGAC

   a     A  R  L  C  S  V  G  H  P  V  F  Q  T  G  A  K  V  T  F  L  -

      CTAGAGTTTGAGTTTAGCTGCTCCTCTCTCCTGAGCCAGGTCTTTGGGAAGCTGACTGCC
2701  ----------+---------+---------+---------+---------+---------+  2760
      GATCTCAAACTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCCTTCGACTGACGG

   a     L  E  F  E  F  S  C  S  S  L  L  S  Q  V  F  G  K  L  T  A  -

      AGCAGTGACAGCCTGGAGAGAAATGGCACCCTTCAAGAAAACACAGCCCAGACCTCAGCC
2761  ----------+---------+---------+---------+---------+---------+  2820
      TCGTCACTGTCGGACCTCTCTTTACCGTGGGAAGTTCTTTTGTGTCGGGTCTGGAGTCGG

   a     S  S  D  S  L  E  R  N  G  T  L  Q  E  N  T  A  Q  T  S  A  -

      TACATCCAATATGAGCCCCACCTCCTGTTCTCTAGTGAGTCTACCCTGCACCGCTATGAG
2821  ----------+---------+---------+---------+---------+---------+  2880
      ATGTAGGTTATACTCGGGGTGGAGGACAAGAGATCACTCAGATGGGACGTGGCGATACTC

   a     Y  I  Q  Y  E  P  H  L  L  F  S  S  E  S  T  L  H  R  Y  E  -

      GTTCACCCATATGGGACCCTCCCAGTGGGTCCTGGCCCAGAATTCAAAACCACTCTCAGG
2881  ----------+---------+---------+---------+---------+---------+  2940
      CAAGTGGGTATACCCTGGGAGGGTCACCCAGGACCGGGTCTTAAGTTTTGGTGAGAGTCC

   a     V  H  P  Y  G  T  L  P  V  G  P  G  P  E  F  K  T  T  L  R  -

      GTTCAGAACCTAGGCTGCTATGTGGTCAGTGGCCTCATCATCTCAGCCCTCCTTCCAGCT
2941  ----------+---------+---------+---------+---------+---------+  3000
      CAAGTCTTGGATCCGACGATACACCAGTCACCGGAGTAGTAGAGTCGGGAGGAAGGTCGA

   a     V  Q  N  L  G  C  Y  V  V  S  G  L  I  I  S  A  L  L  P  A  -

      GTGGCCCATGGGGGCAATTACTTCCTATCACTGTCTCAAGTCATCACTAACAATGCAAGC
3001  ----------+---------+---------+---------+---------+---------+  3060
      CACCGGGTACCCCCGTTAATGAAGGATAGTGACAGAGTTCAGTAGTGATTGTTACGTTCG

   a     V  A  H  G  G  N  Y  F  L  S  L  S  Q  V  I  T  N  N  A  S  -
```

41

```
          TGCATAGTGCAGAACCTGACTGAACCCCCAGGCCCACCTGTGCATCCAGAGGAGCTTCAA
   3061   ---------+---------+---------+---------+---------+---------+   3120
          ACGTATCACGTCTTGGACTGACTTGGGGGTCCGGGTGGACACGTAGGTCTCCTCGAAGTT

     a      C   I   V   Q   N   L   T   E   P   P   G   P   P   V   H   P   E   E   L   Q   -


          CACACAAACAGACTGAATGGGAGCAATACTCAGTGTCAGGTGGTGAGGTGCCACCTTGGG
   3121   ---------+---------+---------+---------+---------+---------+   3180
          GTGTGTTTGTCTGACTTACCCTCGTTATGAGTCACAGTCCACCACTCCACGGTGGAACCC

     a      H   T   N   R   L   N   G   S   N   T   Q   C   Q   V   V   R   C   H   L   G   -


          CAGCTGGCAAAGGGGACTGAGGTCTCTGTTGGACTATTGAGGCTGGTTCACAATGAATTT
   3181   ---------+---------+---------+---------+---------+---------+   3240
          GTCGACCGTTTCCCCTGACTCCAGAGACAACCTGATAACTCCGACCAAGTGTTACTTAAA

     a      Q   L   A   K   G   T   E   V   S   V   G   L   L   R   L   V   H   N   E   F   -


          TTCCGAAGAGCCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTTTGAGCTGGGAACCGAA
   3241   ---------+---------+---------+---------+---------+---------+   3300
          AAGGCTTCTCGGTTCAAGTTCAGGGACTGCCACCAGTCGTGGAAACTCGACCCTTGGCTT

     a      F   R   R   A   K   F   K   S   L   T   V   V   S   T   F   E   L   G   T   E   -


          GAGGGCAGTGTCCTACAGCTGACTGAAGCCTCCCGTTGGAGTGAGAGCCTCTTGGAGGTG
   3301   ---------+---------+---------+---------+---------+---------+   3360
          CTCCCGTCACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTCTCGGAGAACCTCCAC

     a      E   G   S   V   L   Q   L   T   E   A   S   R   W   S   E   S   L   L   E   V   -


          GTTCAGACCCGGCCTATCCTCATCTCCCTGTGGATCCTCATAGGCAGTGTCCTGGGAGGG
   3361   ---------+---------+---------+---------+---------+---------+   3420
          CAAGTCTGGGCCGGATAGGAGTAGAGGGACACCTAGGAGTATCCGTCACAGGACCCTCCC

     a      V   Q   T   R   P   I   L   I   S   L   W   I   L   I   G   S   V   L   G   G   -


          TTGCTCCTGCTTGCTCTCCTTGTCTTCTGCCTGTGGAAGCTTGGCTTCTTTGCCCATAAG
   3421   ---------+---------+---------+---------+---------+---------+   3480
          AACGAGGACGAACGAGAGGAACAGAAGACGGACACCTTCGAACCGAAGAAACGGGTATTC

     a      L   L   L   L   A   L   L   V   F   C   L   W   K   L   G   F   F   A   H   K   -


          AAAATCCCTGAGGAAGAAAAAGAGAAGAGAAGTTGGAGCAATGAATGTAGAATAAGGGT
   3481   ---------+---------+---------+---------+---------+---------+   3540
          TTTTAGGGACTCCTTCTTTTTTCTCTTCTCTTCACCTCGTTACTTACATCTTATTCCCA

     a      K   I   P   E   E   E   K   R   E   E   K   L   E   Q


          CTAGAAAGTCCTCCCTGGCAGCTTTCTTCAAGAGACTTGCATAAAAGCAGAGGTTTGGGG
   3541   ---------+---------+---------+---------+---------+---------+   3600
          GATCTTTCAGGAGGGACCGTCGAAAGAAGTTCTCTGAACGTATTTTCGTCTCCAAACCCC


          GCTCAGATGGGACAAGAAGCCGCCTCTGGACTATCTCCCCAGACCAGCAGCCTGACTTGA
   3601   ---------+---------+---------+---------+---------+---------+   3660
          CGAGTCTACCCTGTTCTTCGGCGGAGACCTGATAGAGGGGTCTGGTCGTCGGACTGAACT


          CTTTTGAGTCCTAGGGATGCTGCTGGCTAGAGATGAGGCTTTACCTCAGACAAGAAGAGC
   3661   ---------+---------+---------+---------+---------+---------+   3720
          GAAAACTCAGGATCCCTACGACGACCGATCTCTACTCCGAAATGGAGTCTGTTCTTCTCG
```

42

```
      TGGCACCAAAACTAGCCATGCTCCCACCCTCTGCTTCCCTCCTCCTCGTGATCCTGGTTC
3721  ---------+---------+---------+---------+---------+---------+ 3780
      ACCGTGGTTTTGATCGGTACGAGGGTGGGAGACGAAGGGAGGAGGAGCACTAGGACCAAG


      CATAGCCAACACTGGGGCTTTTGTTTGGGGTCCTTTTATCCCCAGGAATCAATAATTTTT
3781  ---------+---------+---------+---------+---------+---------+ 3840
      GTATCGGTTGTGACCCCGAAAACAAACCCCAGGAAAATAGGGGTCCTTAGTTATTAAAAA


      TTGCCTAGGAAAAAAAAAAGCGGCCGCGAATTCGATATCAAGCT
3841  ---------+---------+---------+---------+---- 3884
      AACGGATCCTTTTTTTTTTTCGCCGGCGCTTAAGCTATAGTTCGA
```

(2) INFORMATION FOR SEQ ID NO. 2:
    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3779 base pairs
        (B) TYPE: nucleid acid and amino acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
        (E)
    (i)   MOLECULAR TYPE: cDNA
    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: human
        (B)   CELLTYPE: chondrocyte

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

```
        CAGGTCAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTG
     1  ---------+---------+---------+---------+---------+---------+  60
        GTCCAGTCTTTGGCTAGTCCGTACCTTGAGGGGAAGCAGTGAGTGGACAAGAACGGGGAC

                            M  E  L  P  F  V  T  H  L  F  L  P  L  -

        GTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTC
    61  ---------+---------+---------+---------+---------+---------+ 120
        CACAAGGACTGTCCAGAGACGAGGGGGAAATTGGACCTACTTGTAGTGGGTGCGGATAAG

    a      V  F  L  T  G  L  C  S  P  F  N  L  D  E  H  H  P  R  L  F  -

        CCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAG
   121  ---------+---------+---------+---------+---------+---------+ 180
        GGTCCCGGTGGTCTTCGACTTAAACCTATGTCACAGAATGTTGTACAACCCCCACCTGTC

    a      P  G  P  P  E  A  E  F  G  Y  S  V  L  Q  H  V  G  G  Q  -

        CGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
   181  ---------+---------+---------+---------+---------+---------+ 240
        GCTACCTACGACCACCCGCGGGGGACCCTACCCGGAAGTCCGCTGGCCTCCCCCCTGCAA

    a      R  W  M  L  V  G  A  P  W  D  G  P  S  G  D  R  R  G  D  V  -

        TATCGCTGCCCTGTAGGGGGGGGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGAC
   241  ---------+---------+---------+---------+---------+---------+ 300
        ATAGCGACGGGACATCCCCCCCGGGTGTTACGGGGTACACGGTTCCCGGTGAATCCACTG

    a      Y  R  C  P  V  G  G  A  H  N  A  P  C  A  K  G  H  L  G  D  -

        TACCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTA
   301  ---------+---------+---------+---------+---------+---------+ 360
        ATGGTTGACCCTTTAAGTAGAGTAGGACGACACTTATACGTGGACCCCTACAGAGACAAT

    a      Y  Q  L  G  N  S  S  H  P  A  V  N  M  H  L  G  M  S  L  L  -

        GAGACAGATGGTGATGGGGGATTCATGGCCTGTGCCCCTCTCTGGTCTCGTGCTTGTGGC
   361  ---------+---------+---------+---------+---------+---------+ 420
        CTCTGTCTACCACTACCCCCTAAGTACCGGACACGGGGAGAGACCAGAGCACGAACACCG

    a      E  T  D  G  D  G  G  F  M  A  C  A  P  L  W  S  R  A  C  G  -

        AGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGA
   421  ---------+---------+---------+---------+---------+---------+ 480
        TCGAGACAGAAGTCAAGACCCTATACACGGGCACACCTACGAAGTAAGGTCGGAGTCCCT
```

44

```
a    S  S  V  F  S  S  G  I  C  A  R  V  D  A  S  F  Q  P  Q  G  -

     AGCCTGGCACCCACTGCCCAACGCTGCCCAACATACATGGATGTTGTCATTGTCTTGGAT
481  ---------+---------+---------+---------+---------+---------+ 540
     TCGGACCGTGGGTGACGGGTTGCGACGGGTTGTATGTACCTACAACAGTAACAGAACCTA

a    S  L  A  P  T  A  Q  R  C  P  T  Y  M  D  V  V  I  V  L  D  -

     GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGACCTTCCTACGAAGACTGGTAGGG
541  ---------+---------+---------+---------+---------+---------+ 600
     CCGAGGTTGTCGTAGATGGGGACCAGACTTCAAGTCTGGAAGGATGCTTCTGACCATCCC

a    G  S  N  S  I  Y  P  W  S  E  V  Q  T  F  L  R  R  L  V  G  -

     AAACTGTTTATTGACCCAGAACAGATACAGGTGGGACTGGTACAGTATGGGGAGAGCCCT
601  ---------+---------+---------+---------+---------+---------+ 660
     TTTGACAAATAACTGGGTCTTGTCTATGTCCACCCTGACCATGTCATACCCCTCTCGGGA

a    K  L  F  I  D  P  E  Q  I  Q  V  G  L  V  Q  Y  G  E  S  P  -

     GTACATGAGTGGTCCCTGGGAGATTTCCGAACGAAGGAAGAAGTGGTGAGAGCAGCAAAG
661  ---------+---------+---------+---------+---------+---------+ 720
     CATGTACTCACCAGGGACCCTCTAAAGGCTTGCTTCCTTCTTCACCACTCTCGTCGTTTC

a    V  H  E  W  S  L  G  D  F  R  T  K  E  E  V  V  R  A  A  K  -

     AACCTCAGTCGGCGGGAGGGACGAGAAACAAAGACTGCCCAAGCAATAATGGTGGCCTGC
721  ---------+---------+---------+---------+---------+---------+ 780
     TTGGAGTCAGCCGCCCTCCCTGCTCTTTGTTTCTGACGGGTTCGTTATTACCACCGGACG

a    N  L  S  R  R  E  G  R  E  T  K  T  Q  A  I  M  V  A  C  -

     ACAGAAGGGTTCAGTCAGTCCCATGGGGGCCGACCCGAGGCTGCCAGGCTACTGGTGGTT
781  ---------+---------+---------+---------+---------+---------+ 840
     TGTCTTCCCAAGTCAGTCAGGGTACCCCCGGCTGGGCTCCGACGGTCCGATGACCACCAA

a    T  E  G  F  S  Q  S  H  G  G  R  P  E  A  A  R  L  L  V  V  -

     GTCACTGATGGAGAGTCCCATGATGGAGAGGAGCTTCCTGCAGCACTAAAGGCCTGTGAG
841  ---------+---------+---------+---------+---------+---------+ 900
     CAGTGACTACCTCTCAGGGTACTACCTCTCCTCGAAGGACGTCGTGATTTCCGGACACTC

a    V  T  D  G  E  S  H  D  G  E  E  L  P  A  A  L  K  A  C  E  -

     GCTGGAAGAGTGACACGCTATGGGATTGCAGTCCTTGGTCACTACCTCCGGCGGCAGCGA
901  ---------+---------+---------+---------+---------+---------+ 960
     CGACCTTCTCACTGTGCGATACCCTAACGTCAGGAACCAGTGATGGAGGCCGCCGTCGCT

a    A  G  R  V  T  R  Y  G  I  A  V  L  G  H  Y  L  R  R  Q  R  -

     GATCCCAGCTCTTTCCTGAGAGAAATTAGAACTATTGCCAGTGATCCAGTGAGCGATTC
961  ---------+---------+---------+---------+---------+---------+ 1020
     CTAGGGTCGAGAAAGGACTCTCTTTAATCTTGATAACGGTCACTAGGTCTACTCGCTAAG

a    D  P  S  S  F  L  R  E  I  R  T  I  A  S  D  P  D  E  R  F  -

     TTCTTCAATGTCACAGATGAGGCTGCTCTGACTGACATTGTGGATGCACTAGGAGATCGG
1021 ---------+---------+---------+---------+---------+---------+ 1080
     AAGAAGTTACAGTGTCTACTCCGACGAGACTGACTGTAACACCTACGTGATCCTCTAGCC

a    F  F  N  V  T  D  E  A  A  L  T  D  I  V  D  A  L  G  D  R  -

     ATTTTTGGCCTTGAAGGGTCCCATGCAGAAAACGAAAGCTCCTTTGGGCTGGAAATGTCT
1081 ---------+---------+---------+---------+---------+---------+ 1140
     TAAAAACCGGAACTTCCCAGGGTACGTCTTTTGCTTTCGAGGAAACCCGACCTTTACAGA
```

45

```
a        I  F  G  L  E  G  S  H  A  E  N  E  S  S  F  G  L  E  M  S  -

         CAGATTGGTTTCTCCACTCATCGGCTAAAGGATGGGATTCTTTTTGGGATGGTGGGGGCC
    1141 ---------+---------+---------+---------+---------+---------+ 1200
         GTCTAACCAAAGAGGTGAGTAGCCGATTTCCTACCCTAAGAAAAACCCTACCACCCCCGG

a        Q  I  G  F  S  T  H  R  L  K  D  G  I  L  F  G  M  V  G  A  -

         TATGACTGGGGAGGCTCTGTGCTATGGCTTGAAGGAGGCCACCGCCTTTTCCCCCCACGA
    1201 ---------+---------+---------+---------+---------+---------+ 1260
         ATACTGACCCCTCCGAGACACGATACCGAACTTCCTCCGGTGGCGGAAAAGGGGGGTGCT

a        Y  D  W  G  S  V  L  W  L  E  G  G  H  R  L  F  P  P  R  -

         ATGGCACTGGAACACGAGTTCCCCCCTGCACTGCAGAACCATGCAGCCTACCTGGGTTAC
    1261 ---------+---------+---------+---------+---------+---------+ 1320
         TACCGTGACCTTCTGCTCAAGGGGGGACGTGACGTCTTGGTACGTCGGATGGACCCAATG

a        M  A  L  E  D  E  F  P  P  A  L  Q  N  H  A  A  Y  L  G  Y  -

         TCTGTTTCTTCCATGCTTTTGCGGGGTGGACGCCGCCTGTTTCTCTCTGGGGCTCCTCGA
    1321 ---------+---------+---------+---------+---------+---------+ 1380
         AGACAAAGAAGGTACGAAAACGCCCCACCTGCGGCGGACAAAGAGAGACCCCGAGGAGCT

a        S  V  S  S  M  L  L  R  G  G  R  R  L  F  L  S  G  A  P  R  -

         TTTAGACATCGAGGAAAAGTCATCGCCTTCCAGCTTAAGAAAGATGGGGCTGTGAGGGTT
    1381 ---------+---------+---------+---------+---------+---------+ 1440
         AAATCTGTAGCTCCTTTTCAGTAGCGGAAGGTCGAATTCTTTCTACCCCGACACTCCCAA

a        F  R  H  R  G  K  V  I  A  F  Q  L  K  K  D  G  A  V  R  V  -

         GCCCAGAGCCTCCAGGGGGAGCAGATTGGTTCATACTTTGGCAGTGAGCTCTGCCCATTG
    1441 ---------+---------+---------+---------+---------+---------+ 1500
         CGGGTCTCGGAGGTCCCCCTCGTCTAACCAAGTATGAAACCGTCACTCGAGACGGGTAAC

a        A  Q  S  L  Q  G  E  Q  I  G  S  Y  F  G  S  E  L  C  P  L  -

         GATACAGATAGGGATGGAACAACTGATGTCTTACTTGTGGCTGCCCCCATGTTCCTGGGA
    1501 ---------+---------+---------+---------+---------+---------+ 1560
         CTATGTCTATCCCTACCTTGTTGACTACAGAATGAACACCGACGGGGGTACAAGGACCCT

a        D  T  D  R  D  G  T  T  D  V  L  L  V  A  A  P  M  F  L  G  -

         CCCCAGAACAAGGAAACAGGACGTGTTTATGTGTATCTGGTAGGCCAGCAGTCCTTGCTG
    1561 ---------+---------+---------+---------+---------+---------+ 1620
         GGGGTCTTGTTCCTTTGTCCTGCACAAATACACATAGACCATCCGGTCGTCAGGAACGAC

a        P  Q  N  K  E  T  G  R  V  Y  V  Y  L  V  G  Q  Q  S  L  L  -

         ACCCTCCAAGGAACACTTCAGCCAGAACCCCCCCAGGATGCTCGGTTTGGCTTTGCCATG
    1621 ---------+---------+---------+---------+---------+---------+ 1680
         TGGGAGGTTCCTTGTGAAGTCGGTCTTGGGGGGGTCCTACGAGCCAAACCGAAACGGTAC

a        T  L  Q  G  T  L  Q  P  E  P  P  Q  D  A  R  F  G  F  A  M  -

         GGAGCTCTTCCTGATCTGAACCAAGATGGTTTTGCTGATGTGGCTGTGGGGGCGCCTCTG
    1681 ---------+---------+---------+---------+---------+---------+ 1740
         CCTCGAGAAGGACTAGACTTGGTTCTACCAAAACGACTACACCGACACCCCCGCGGAGAC

a        G  A  L  P  D  L  N  Q  D  G  F  A  D  V  A  V  G  A  P  L  -

         GAAGATGGGCACCAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCCC
    1741 ---------+---------+---------+---------+---------+---------+ 1800
         CTTCTACCCGTGGTCCCTCGTGACATGGACATGGTACCTTGGGTCTCACCTCAGTCCGGG
```

46

```
a        E  D  G  H  Q  G  A  L  Y  L  Y  H  G  T  Q  S  G  V  R  P    -

         CATCCTGCCCAGAGGATTGCTGCTGCCTCCATGCCACATGCCCTCAGCTACTTTGGCCGA
    1801 ---------+---------+---------+---------+---------+---------+ 1860
         GTAGGACGGGTCTCCTAACGACGACGGAGGTACGGTGTACGGGAGTCGATGAAACCGGCT


a        H  P  A  Q  R  I  A  A  A  S  M  P  H  A  L  S  Y  F  G  R    -

         AGTGTGGATGGTCGGCTAGATCTGGATGGAGATGATCTGGTCGATGTGGCTGTGGGTGCC
    1861 ---------+---------+---------+---------+---------+---------+ 1920
         TCACACCTACCAGCCGATCTAGACCTACCTCTACTAGACCAGCTACACCGACACCCACGG


a        S  V  D  G  R  L  D  L  D  G  D  D  L  V  D  V  A  V  G  A    -

         CAGGGGGCAGCCATCCTGCTCAGCTCCCGGCCCATTGTCCATCTGACCCCATCACTGGAG
    1921 ---------+---------+---------+---------+---------+---------+ 1980
         GTCCCCCGTCGGTAGGACGAGTCGAGGGCCGGGTAACAGGTAGACTGGGGTAGTGACCTC


a        Q  G  A  A  I  L  L  S  R  P  I  V  H  L  T  P  S  L  E      -

         GTGACCCCACAGGCCATCAGTGTGGTTCAGAGGGACTGTAGGCGGCGAGGCCAAGAAGCA
    1981 ---------+---------+---------+---------+---------+---------+ 2040
         CACTGGGGTGTCCGGTAGTCACACCAAGTCTCCCTGACATCCGCCGCTCCGGTTCTTCGT


a        V  T  P  Q  A  I  S  V  V  Q  R  D  C  R  R  R  G  Q  E  A    -

         GTCTGTCTGACTGCAGCCCTTTGCTTCCAAGTGACCTCCCGTACTCCTGGTCGCTGGGAT
    2041 ---------+---------+---------+---------+---------+---------+ 2100
         CAGACAGACTGACGTCGGGAAACGAAGGTTCACTGGAGGGCATGAGGACCAGCGACCCTA


a        V  C  L  T  A  A  L  C  F  Q  V  T  S  R  T  P  G  R  W  D    -

         CACCAATTCTACATGAGGTTCACCGCATCACTGGATGAATGGACTGCTGGGGCACGTGCA
    2101 ---------+---------+---------+---------+---------+---------+ 2160
         GTGGTTAAGATGTACTCCAAGTGGCGTAGTGACCTACTTACCTGACGACCCCGTGCACGT


a        H  Q  F  Y  M  R  F  T  A  S  L  D  E  W  T  A  G  A  R  A    -

         GCATTTGATGGCTCTGGCCAGAGGTTGTCCCCTCGGAGGCTCCGGCTCAGTGTGGGGAAT
    2161 ---------+---------+---------+---------+---------+---------+ 2220
         CGTAAACTACCGAGACCGGTCTCCAACAGGGGAGCCTCCGAGGCCGAGTCACACCCCTTA


a        A  F  D  G  S  G  Q  R  L  S  P  R  R  L  R  L  S  V  G  N    -

         GTCACTTGTGAGCAGCTACACTTCCATGTGCTGGATACATCAGATTACCTCCGGCCAGTG
    2221 ---------+---------+---------+---------+---------+---------+ 2280
         CAGTGAACACTCGTCGATGTGAAGGTACACGACCTATGTAGTCTAATGGAGGCCGGTCAC


a        V  T  C  E  Q  L  H  F  H  V  L  D  T  S  D  Y  L  R  P  V    -

         GCCTTGACTGTGACCTTTGCCTTGGACAATACTACAAAGCCAGGGCCTGTGCTGAATGAG
    2281 ---------+---------+---------+---------+---------+---------+ 2340
         CGGAACTGACACTGGAAACGGAACCTGTTATGATGTTTCGGTCCCGGACACGACTTACTC


a        A  L  T  V  T  F  A  L  D  N  T  T  K  P  G  P  V  L  N  E    -

         GGCTCACCCACCTCTATACAAAAGCTGGTCCCCTTCTCAAAGGATTGTGGCCCTGACAAT
    2341 ---------+---------+---------+---------+---------+---------+ 2400
         CCGAGTGGGTGGAGATATGTTTTCGACCAGGGGAAGAGTTTCCTAACACCGGGACTGTTA


a        G  S  P  T  S  I  Q  K  L  V  P  F  S  K  D  C  G  P  D  N    -

         GAATGTGTCACAGACCTGGTGCTTCAAGTGAATATGGACATCAGAGGCTCCAGGAAGGCC
    2401 ---------+---------+---------+---------+---------+---------+ 2460
         CTTACACAGTGTCTGGACCACGAAGTTCACTTATACCTGTAGTCTCCGAGGTCCTTCCGG
```

```
a       E   C   V   T   D   L   V   L   Q   V   N   M   D   I   R   G   S   R   K   A   -

        CCATTTGTGGTTCGAGGTGGCCGGCGGAAAGTGCTGGTATCTACAACTCTGGAGAACAGA
2461    ---------+---------+---------+---------+---------+---------+ 2520
        GGTAAACACCAAGCTCCACCGGCCGCCTTTCACGACCATAGATGTTGAGACCTCTTGTCT

a       P   F   V   V   R   G   G   R   R   K   V   L   V   S   T   T   L   E   N   R   -

        AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTTCTCTAGAAACCTCCACCTGGCC
2521    ---------+---------+---------+---------+---------+---------+ 2580
        TTCCTTTTACGAATGTTATGCTCGGACTCATAGTAGAAGAGATCTTTGGAGGTGGACCGG

a       K   E   N   A   Y   N   T   S   L   S   I   I   F   S   R   N   L   H   L   A   -

        AGTCTCACTCCTCAGAGAGAGAGCCCAATAAAGGTGGAATGTGCCGCCCCTTCTGCTCAT
2581    ---------+---------+---------+---------+---------+---------+ 2640
        TCAGAGTGAGGAGTCTCTCTCTCGGGTTATTTCCACCTTACACGGCGGGGAAGACGAGTA

a       S   L   T   P   Q   R   E   S   P   I   K   V   E   C   A   A   P   S   A   H   -

        GCCCGGCTCTGCAGTGTGGGGCATCCTGTCTTCCAGACTGGAGCCAAGGTGACCTTTCTG
2641    ---------+---------+---------+---------+---------+---------+ 2700
        CGGGCCGAGACGTCACACCCCGTAGGACAGAAGGTCTGACCTCGGTTCCACTGGAAAGAC

a       A   R   L   C   S   V   G   H   P   V   F   Q   T   G   A   K   V   T   F   L   -

        CTAGAGTTTGAGTTTAGCTGCTCCTCTCTCCTGAGCCAGGTCTTTGGGAAGCTGACTGCC
2701    ---------+---------+---------+---------+---------+---------+ 2760
        GATCTCAAACTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCCTTCGACTGACGG

a       L   E   F   E   F   S   C   S   S   L   L   S   Q   V   F   G   K   L   T   A   -

        AGCAGTGACAGCCTGGAGAGAAATGGCACCCTTCAAGAAAACACAGCCCAGACCTCAGCC
2761    ---------+---------+---------+---------+---------+---------+ 2820
        TCGTCACTGTCGGACCTCTCTTTACCGTGGGAAGTTCTTTTGTGTCGGGTCTGGAGTCGG

a       S   S   D   S   L   E   R   N   G   T   L   Q   E   N   T   A   Q   T   S   A   -

        TACATCCAATATGAGCCCCACCTCCTGTTCTCTAGTGAGTCTACCCTGCACCGCTATGAG
2821    ---------+---------+---------+---------+---------+---------+ 2880
        ATGTAGGTTATACTCGGGGTGGAGGACAAGAGATCACTCAGATGGGACGTGGCGATACTC

a       Y   I   Q   Y   E   P   H   L   L   F   S   S   E   S   T   L   H   R   Y   E   -

        GTTCACCCATATGGGACCCTCCCAGTGGGTCCTGGCCCAGAATTCAAAACCACTCTCAGG
2881    ---------+---------+---------+---------+---------+---------+ 2940
        CAAGTGGGTATACCCTGGGAGGGTCACCCAGGACCGGGTCTTAAGTTTTGGTGAGAGTCC

a       V   H   P   Y   G   T   L   P   V   G   P   G   P   E   T   K   T   T   L   R   -

        ACTAACAATGCAAGCTGCATAGTGCAGAACCTGACTGAACCCCCAGGCCCACCTGTGCAT
2941    ---------+---------+---------+---------+---------+---------+ 3000
        TGATTGTTACGTTCGACGTATCACGTCTTGGACTGACTTGGGGGTCCGGGTGGACACGTA

a       T   N   N   A   S   C   I   V   Q   N   L   T   E   P   P   G   P   P   V   H   -

        CCAGAGGAGCTTCAACACACAAACAGACTGAATGGGAGCAATACTCAGTGTCAGGTGGTG
3001    ---------+---------+---------+---------+---------+---------+ 3060
        GGTCTCCTCGAAGTTGTGTGTTTGTCTGACTTACCCTCGTTATGAGTCACAGTCCACCAC

a       P   E   E   L   Q   H   T   N   R   L   N   G   S   N   T   Q   C   Q   V   V   -

        AGGTGCCACCTTGGGCAGCTGGCAAAGGGGACTGAGGTCTCTGTTGGACTATTGAGGCTG
3061    ---------+---------+---------+---------+---------+---------+ 3120
        TCCACGGTGGAACCCGTCGACCGTTTCCCCTGACTCCAGAGACAACCTGATAACTCCGAC
```

48

```
a        R  C  H  L  G  Q  L  A  K  G  T  E  V  S  V  G  L  L  R  L   -

         GTTCACAATGAATTTTTCCGAAGAGCCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTTT
   3121  ---------+---------+---------+---------+---------+---------+  3180
         CAAGTGTTACTTAAAAAGGCTTCTCGGTTCAAGTTCAGGGACTGCCACCAGTCGTGGAAA

a        V  H  N  E  F  F  R  R  A  K  F  K  S  L  T  V  V  S  T  F   -

         GAGCTGGGAACCGAAGAGGGCAGTGTCCTACAGCTGACTGAAGCCTCCCGTTGGAGTGAG
   3181  ---------+---------+---------+---------+---------+---------+  3240
         CTCGACCCTTGGCTTCTCCCGTCACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTC

a        E  L  G  T  E  E  G  S  V  L  Q  L  T  E  A  S  R  W  S  E   -

         AGCCTCTTGGAGGTGGTTCAGACCCGGCCTATCCTCATCTCCCTGTGGATCCTCATAGGC
   3241  ---------+---------+---------+---------+---------+---------+  3300
         TCGGAGAACCTCCACCAAGTCTGGGCCGGATAGGAGTAGAGGGACACCTAGGAGTATCCG

a        S  L  L  E  V  V  Q  T  R  P  I  L  I  S  L  W  I  L  I  G   -

         AGTGTCCTGGGAGGGTTGCTCCTGCTTGCTCTCCTTGTCTTCTGCCTGTGGAAGCTTGGC
   3301  ---------+---------+---------+---------+---------+---------+  3360
         TCACAGGACCCTCCCAACGAGGACGAACGAGAGGAACAGAAGACGGACACCTTCGAACCG

a        S  V  L  G  G  L  L  L  L  L  L  V  F  C  L  W  K  L  G   -

         TTCTTTGCCCATAAGAAAATCCCTGAGGAAGAAAAAAGAGAAGAGAAGTTGGAGCAATGA
   3361  ---------+---------+---------+---------+---------+---------+  3420
         AAGAAACGGGTATTCTTTTAGGGACTCCTTCTTTTTTCTCTTCTCTTCAACCTCGTTACT

a        F  F  A  H  K  K  I  P  E  E  E  K  R  E  E  K  L  E  Q

         ATGTAGAATAAGGGTCTAGAAAGTCCTCCCTGGCAGCTTTCTTCAAGAGACTTGCATAAA
   3421  ---------+---------+---------+---------+---------+---------+  3480
         TACATCTTATTCCCAGATCTTTCAGGAGGGACCGTCGAAAGAAGTTCTCTGAACGTATTT

         AGCAGAGGTTTGGGGGCTCAGATGGGACAAGAAGCCGCCTCTGGACTATCTCCCCAGACC
   3481  ---------+---------+---------+---------+---------+---------+  3540
         TCGTCTCCAAACCCCCGAGTCTACCCTGTTCTTCGGCGGAGACCTGATAGAGGGGTCTGG

         AGCAGCCTGACTTGACTTTTGAGTCCTAGGGATGCTGCTGGCTAGAGATGAGGCTTTACC
   3541  ---------+---------+---------+---------+---------+---------+  3600
         TCGTCGGACTGAACTGAAAACTCAGGATCCCTACGACGACCGATCTCTACTCCGAAATGG

         TCAGACAAGAAGAGCTGGCACCAAAACTAGCCATGCTCCCACCCTCTGCTTCCCTCCTCC
   3601  ---------+---------+---------+---------+---------+---------+  3660
         AGTCTGTTCTTCTCGACCGTGGTTTTGATCGGTACGAGGGTGGGAGACGAAGGGAGGAGG

         TCGTGATCCTGGTTCCATAGCCAACACTGGGGCTTTTGTTTGGGGTCCTTTTATCCCCAG
   3661  ---------+---------+---------+---------+---------+---------+  3720
         AGCACTAGGACCAAGGTATCGGTTGTGACCCCGAAAACAAACCCCAGGAAAATAGGGGTC

         GAATCAATAATTTTTTTGCCTAGGAAAAAAAAAAGCGGCCGCGAATTCGATATCAAGCT
   3721  ---------+---------+---------+---------+---------+------+---------  3779
         CTTAGTTATTAAAAAAACGGATCCTTTTTTTTTTCGCCGGCGCTTAAGCTATAGTTCGA
```

49

(2) INFORMATION FOR SEQ ID NO. 3:

    (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 143 base pairs
          (B) TYPE: nucleic acid and amino acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (iii) MOLECULAR TYPE: cDNA
    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: human
          (B) CELLTYPE: chondrocyte

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

```
        NdeI
         |
      GGGGCATATGGTTCAGAACCTGGGTTGCTACGTTGTTTCCGGTCTGATCATCTCCGCTCT
   1  ---------+---------+---------+---------+---------+---------+  60
      CCCCGTATACCAAGTCTTGGACCCAACGATGCAACAAAGGCCAGACTAGTAGAGGCGAGA

b       G  H  M  V  Q  N  L  G  C  Y  V  V  S  G  L  I  I  S  A  L  -

      GCTGCCGGCTGTTGCTCACGGTGGTAACTACTTCCTAAGCTTGTCCCAGGTTATCAGCGG
  61  ---------+---------+---------+---------+---------+---------+  120
      CGACGGCCGACAACGAGTGCCACCATTGATGAAGGATTCGAACAGGGTCCAATAGTCGCC

b       L  P  A  V  A  H  G  G  N  Y  F  L  S  L  S  Q  V  I  S  G  -

        BamHI
          |
      CCTGGTGCCGCGCGGATCCCCCC
 121  ---------+---------+---  143
      GGACCACGGCGCGCCTAGGGGGG

b       L  V  P  R  G  S  P  -
```